

"Express Mail" mailing label number EL 856 154 676 US. I hereby certify that this document and referenced attachments are being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR § 1.10 on the date indicated and is addressed to: Commissioner for Patents, Box Patent Application, Washington, D.C. 20231 on April 16, 2001.

By: Nancy Ramos Printed: Nancy Ramos

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Bandman et al.

Title: **HUMAN EXTRACELLULAR MATRIX PROTEINS**

Serial No.: **To Be Assigned** Filing Date: **Herewith**

Examiner: **To Be Assigned** Group Art Unit: **To Be Assigned**

Official Draftsman

Commissioner for Patents
Washington, D.C. 20231

SUBMISSION OF FORMAL DRAWINGS

Sir:

Transmitted herewith are Figure(s) 1A, 1B, 1C, 1D, 1E, 1F, 1G, 2A, 2B, 2C, 2D, 2E, 3A, 3B, 4A, 4B, and 4C, as seventeen (17) sheets of formal drawings for this application. Each sheet of drawing indicates the identifying indicia suggested in 37 CFR Section 1.84(c) on the reverse side of the drawings.

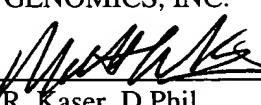
Applicants believe that no fee is due with this paper. However, if the Commissioner determines that a fee is necessary, the Commissioner is hereby authorized to charge any additional fees associated with this communication or credit any overpayment to Deposit Account No. **09-0108**. A **duplicate copy of this communication is enclosed**.

If there are any questions regarding the above, the Examiner is invited to call the undersigned at 650-855-0555.

Respectfully submitted,

INCYTE GENOMICS, INC.

Date: 16th April 2001


Matthew R. Kaser, D.Phil.
Reg. No. 44,817
Direct Dial Telephone: (650) 845-4596

3160 Porter Drive
Palo Alto, California 94304
Phone: (650) 855-0555
Fax: (650) 845-4166

CCA	AGA	TTC	TTC	TGA	GGA	GTC	TAG	CCA	GGT	GGT	GAG	CCG	TGT	AAT	CTG	AAC	CAG
9	18	27	36	45	54												
63	72	81	90	99	108												
CTG	TGT	CCA	GAC	TGA	GGC	CCC	ATT	TGC	ATT	ATT	TAA	CAT	ACT	TAG	AAA	ATG	AAG
117	126	135	144	153	162												
TGT	TCA	TTT	TTA	ACA	TTC	CTC	CTC	CAA	TTG	GGT	TAA	TGC	TGA	ATT	ACT	GAA	GAG
171	180	189	198	207	216												
GGC	TAA	GCA	AAA	CCA	GGT	GCT	GTC	GAG	GGC	TCT	GCA	GTG	GCT	GGG	AGG	ACC	
225	234	243	252	261	270												
CCG	GCG	CTC	TCC	CCG	TGT	CCT	CTC	CAC	GAC	TCG	CTC	GGC	CCC	TCT	GGA	ATA	AAA
279	288	297	306	315	324												
CAC	CCG	CGA	GCC	CCG	AGG	GCC	CAG	AGG	AGG	CCG	ACG	TGC	CCG	AGC	TCC	TCC	GGG
333	342	351	360	369	378												
GGT	CCC	GCC	CGC	GAG	CTT	TCT	TCT	CGC	CTT	CGC	ATC	TCC	TCC	TCG	CGC	GTC	TTC
387	396	405	414	423	432												
GAC	ATG	CCA	GGA	ATA	AAA	AGG	ATA	CTC	ACT	GTG	ACC	ATT	CTG	GCT	CTC	TGT	CTT
M	P	G	I	K	R	I	L	T	V	T	I	L	A	L	C	L	

FIGURE 1A

CCA	AGC	CCT	GGG	AAT	GCA	CAG	GCA	CAG	TGC	ACG	AAT	GGC	TTT	GAC	CTG	GAT	CGC
P	S	P	G	N	A	Q	A	Q	C	T	N	G	F	D	L	D	R
441		450		459		468		477		486							
CAG	TCA	GGG	CAG	TGT	TTA	GAT	ATT	GAT	GAA	TGC	CGA	ACC	ATC	CCC	GAG	GCC	TGC
Q	S	G	Q	C	L	D	I	D	E	C	R	T	I	P	E	A	C
495		504		513		522		531		540							
CGA	GGA	GAC	ATG	ATG	TGT	GTT	AAC	CAA	AAT	GGC	GGG	TAT	TTA	TGC	ATT	CCC	CGG
R	G	D	M	M	C	V	N	Q	N	G	G	Y	L	C	I	P	R
549		558		567		576		585		594							
CGA	GGG	GAC	ATG	ATG	TGT	GTT	AAC	CAA	AAT	GGC	GGG	TAT	TTA	TGC	ATT	CCC	CGG
T	N	P	V	Y	R	G	P	Y	S	N	P	Y	L	C	I	P	R
603		612		621		630		639		648							
ACA	AAC	CCT	GTG	TAT	CGA	GGG	CCC	TAC	TCG	AAC	CCC	TAC	TCG	ACC	CCC	TAC	TCA
T	N	P	V	Y	R	G	P	Y	S	N	P	Y	S	T	P	Y	S
657		666		675		684		693		702							
GGT	CCG	TAC	CCA	GCA	GCT	GCC	CCA	CCA	CTC	TCA	GCT	CCA	AAC	TAT	CCC	ACG	ATC
G	P	Y	P	A	A	A	P	P	L	S	A	P	N	Y	P	T	I
711		720		729		738		747		756							
TCC	AGG	CTT	ATA	TGC	CGC	TTT	GGA	TAC	CAG	ATG	GAT	GAA	AGC	AAC	CAA	TGT	
S	R	P	L	I	C	R	F	G	Y	Q	M	D	E	S	N	Q	C
765		774		783		792		801		810							
GTG	GAT	GTG	GAC	GAG	TGT	GCA	ACA	GAT	TCC	CAC	CAG	TGC	AAC	CCC	ACC	CAG	ATC
V	D	V	D	E	C	A	T	D	S	H	Q	C	N	P	T	Q	I

FIGURE 1B

FIGURE 1C

TTC	TGC	TCC	TGC	CCT	CCA	GGC	TAC	ATC	CTG	CTG	GAT	GAC	AAC	CGA	AGC	TGC	CAA	1242
F	C	S	C	P	P	G	Y	I	L	L	D	D	N	R	S	C	Q	
1197		1206		1215		1224		1269		1278		1287		1296		1333		1242
GAC	ATC	AAC	GAA	TGT	GAG	CAC	AGG	AAC	CAC	ACG	TGC	AAC	CTG	CAG	CAG	ACG	TGC	
D	I	N	E	C	E	H	R	N	H	T	C	N	L	Q	Q	T	C	
1251		1260		1305		1314		1323		1332		1341		1350		1350		1296
TAC	AAT	TTA	CAA	GGG	GGC	TTC	AAA	TGC	ATC	GAC	CCC	ATC	CGC	TGT	GAG	GAG	CCT	
Y	N	L	Q	G	G	F	K	C	I	D	P	I	R	C	E	E	P	
1359		1368		1359		1368		1377		1386		1395		1404		1350		1296
TAT	CTG	AGG	ATC	AGT	GAT	AAC	CGC	TGT	ATG	TGT	CCT	GCT	GAG	AAC	CCT	GGC	TGC	
Y	L	R	I	S	D	N	R	C	M	C	P	A	E	N	P	G	C	
1413		1422		1413		1431		1440		1449		1449		1458		1458		1296
AGA	GAC	CAG	CCC	TTT	ACC	ATC	T ^T GT	TAC	CGG	GAC	ATG	GAC	GTG	GTG	TCA	GGA	CGC	
R	D	Q	P	F	T	I	L	Y	R	D	M	D	V	V	S	G	R	
1467		1476		1467		1485		1485		1494		1503		1512		1512		1296
TCC	GTT	CCC	GCT	GAC	ATC	TTC	CAA	ATG	CAA	GCC	ACG	ACC	CGC	TAC	CCT	GGG	GCC	
S	V	P	A	D	I	F	Q	M	Q	A	T	T	R	Y	P	G	A	
1521		1530		1521		1539		1539		1548		1557		1566		1566		1296
TAT	TAC	ATT	TTC	CAG	ATC	AAA	TCT	GGG	AAT	GAG	GGC	AGA	GAA	TTT	TAC	ATG	CGG	
Y	Y	I	F	Q	I	K	S	G	N	E	G	R	E	F	Y	M	R	

FIGURE 1D

CAA	ACG	GGC	CCC	ATC	AGT	GCC	ACC	CTG	GTG	ATG	ACA	CGC	CCC	ATC	AAA	GGG	CCC	1620
Q	T	G	P	I	S	A	T	L	V	M	T	R	P	I	K	G	P	
1575	1584			1593				1602				1611						1620
CGG	GAA	ATC	CAG	CTG	GAC	TTG	GAA	ATG	ATC	ACT	GTC	AAC	ACT	GTC	ATC	AAC	TTC	1674
R	E	I	Q	L	D	L	E	M	I	T	V	N	T	V	I	N	F	
1629	1638			1647				1656				1665						1674
AGA	GGC	AGC	TCC	GTG	ATC	CGA	CTG	CGG	ATA	TAT	GTG	TCG	CAG	TAC	CCA	TTC	TGA	1728
R	G	S	S	V	I	R	L	R	I	Y	V	S	Q	Y	P	F		
1683	1692			1701				1710				1719						1728
GCC	TCG	GGC	TGG	AGC	CTC	CGA	CGC	TGC	CTC	TCA	TTG	GCA	CCA	AGG	GAC	AGG	AGA	
1737	1746			1755				1764				1773						1782
1791	1800			1809				1818				1827						1836
TGA	ACG	GAA	ATA	ACA	GAG	AGA	ATG	AGA	GCG	ACA	CAG	ACG	TTA	GGC	ATT	TCC	TGC	
1845	1854			1863				1872				1881						1890
GCA	GAC	CTG	TCA	CCC	CGA	AGA	GTC	AGC	CCC	GAC	TTC	CTG	ACT	CTC	ACC	TGT	ACT	ATT
1899	1908			1917				1926				1935						1944
CAA	AAA	GTA	TAA	TCA	TTG	CTC	CCC	TGA	TAG	AAG	ATT	GTT	GGT	GAA	TTT	TCA	AGG	

FIGURE 1E

2007 2016 2025 2034 2043 2052
CCT TCA GTT TAT TTC CAC TAT TTT CAA AGA AAA TAG ATT AGG TTT GCG GGG GTC

2061 2070 2079 2088 2097 2106
TGA GTC TAT GTT CAA AGA CTG TGA ACA GCT TGC TGT CAC TTC TTC ACC TCT TCC

2115 2124 2133 2142 2151 2160
ACT CCT TCT CTC ACT GTG TTA CTG CTT TGC AAA GAC CCG GGA GCT GGC GGG GAA

2169 2178 2187 2196 2205 2214
CCC TGG GAG TAG CTA GTT TGC TTT TTG CGT ACA CAG AGA AGG CTA TGT AAA CAA

2223 2232 2241 2250 2259 2268
ACC ACA GCA GGA TCG AAG GGT TTT TAG AGA ATG TGT TTC AAA ACC ATG CCT GGT

2277 2286 2295 2304 2313 2322
ATT TTC AAC CAT AAA AGA AGT TTC AGT TGT CCT TAA ATT TGT ATA ACG GTT TAA

2331 2340 2349 2358 2367 2376
TTC TGT CTT CAT TTT GAG TAT TTT TAA AAA ATA TGT CGT AGA ATT CCT TCG

2385 2394 2403 2412 2421 2430
AAA GGC CTT CAG ACA CAT GCT ATG TTC TGT CTT CCC AAA CCC AGT CTC CTC TCC

2439 2448 2457 2466 2475 2484
ATT TTA GCC CAG TGT TTT CTT TGA GGA CCC CTT AAT CTT GCT TTC TTT AGA ATT

FIGURE 1F

FIGURE 1G

2493 2502 2511 2520 2529 2538
TTT ACC CAA TTG GAT TGG AAT GCA GAG GTC TCC AAA CTG ATT AAA TAT TTG AAG
2547
AGA AAA AAA AAA

9	18	27	36	45	54
TG	GGT	GCA	AGC	TCA	CAA
CCG	TAA	CAG	CCA	CCA	GAC
AAG	CTT	CAG	CTT	CAG	TGG
CTT	CAC	ATC	ACT	TGC	CCG
CTG	AGG	ATG	GGG	ACC	ACA
M	G	T	T	A	R
117	126	135	144	153	162
GCT	CCC	AGG	ATG	GGG	ACC
TCT	GGC	TCT	GAG	GCA	GCC
G	A	A	S	E	A
V	A	S	A	A	R
171	180	189	198	207	216
GTT	GCT	TCT	GCT	GGA	GGC
T	A	S	E	G	F
G	A	A	G	G	T
225	234	243	252	261	270
AGG	CCA	GAG	CAC	TTT	CAA
R	P	E	H	F	Q
279	288	297	306	315	324
TCC	CGA	AGC	CTC	CCC	ATG
S	R	S	L	P	M
333	342	351	360	369	378
GAG	GGA	CAG	AGT	CAA	GTG
E	G	Q	S	Q	V

FIGURE 2A

387	CAG	GAA	AAG	CTG	CTA	CCT	GCC	CAA	CTC	CCT	GCT	GAA	AAG	GAA	GTG	GGT	CCC	CCT	423
Q	E	K	L	L	P	A	Q	L	P	A	E	K	E	V	G	P	P	P	432
441	CTC	CCT	CAG	GAA	GCT	GTC	CCC	CTC	CAA	AAA	GAG	CTG	CCC	TCT	CTC	CAG	CAC	CCC	486
L	P	Q	E	A	V	P	L	Q	K	E	L	P	S	L	Q	H	P	P	
495	AAT	GAA	CAG	AAG	GAA	GGA	ATG	CCA	GCT	CCA	TTT	GGG	GAC	CAG	AGC	CAT	CCA	GAA	540
N	E	Q	K	E	G	M	P	A	P	F	G	D	Q	S	H	P	E	E	
549	CCT	GAG	TCC	TGG	AAT	GCA	GCC	CAG	CAC	TGC	CAA	CAG	GAC	CGG	TCC	CAA	GGG	GGC	594
P	E	S	W	N	A	A	Q	H	C	Q	Q	D	R	S	Q	G	G	G	
603	TGG	GGC	CAC	CGG	CTG	GAT	GGC	TTC	CCC	CCT	GGG	CGG	CCT	TCT	CCA	GAC	AAT	CTG	648
W	G	H	R	L	D	G	F	P	P	G	R	P	S	P	D	N	L	L	
657	AAC	CAA	ATC	TGC	CTT	CCT	AAC	CGT	CAG	CAT	GTG	GTA	TAT	GGT	CCC	TGG	AAC	CTA	702
N	Q	I	C	L	P	N	R	Q	H	V	V	Y	G	P	W	N	L	L	
711	CCA	CAG	TCC	AGC	TAC	TCC	CAC	CTC	ACT	CGC	CAG	GGT	GAG	ACC	CTC	AAT	TTC	CTG	756
P	Q	S	S	Y	S	H	L	T	R	Q	G	E	T	L	N	F	L	L	

FIGURE 2B

GAG	ATT	GGA	TAT	TCC	CGC	TGC	TGC	CAC	CGC	AGC	CAC	ACA	AAC	CGC	CTA	GAG
E	I	G	Y	S	R	C	C	H	C	R	S	H	T	N	R	L
C	A	K	L	V	W	E	E	A	M	S	R	F	C	E	A	F
819	828	837	846	783	792	846	855	801	810							
TGT	GCC	AAA	CTT	GTG	TGG	GAG	GAA	GCA	ATG	AGC	CGA	TTC	TGT	GAG	GCC	GAG
C	S	V	K	T	R	P	H	W	C	C	T	R	Q	G	E	TTC
873	882	891	900	909	918	927	936	945	954	963	972	981	999	1008	1017	1026
TCG	GTC	AAG	ACC	CGA	CCC	CAC	TGG	TGC	ACG	CGG	CAG	GGG	GAG	GCT	CGG	TTC
S	S	C	F	Q	E	E	A	P	Q	P	H	Y	Q	L	R	F
927	936	945	954	945	954	972	990	999	1008	1017	1026	1035	1044	1053	1062	1071
TCC	TGC	TTC	CAG	GAG	GAA	GCT	CCC	CAG	CCA	CAC	TAC	CAG	CTC	CGG	GCC	TGC
S	S	S	C	F	Q	E	A	P	Q	P	H	Y	Q	L	R	C
990	999	1008	1017	1026	1035	1044	1053	1062	1071	1080	1089	1098	1107	1116	1125	1134
AGC	CAT	CAG	CCT	GAT	ATT	TCC	TGC	GGT	CTT	GAG	CTG	CCT	TTC	CCT	GGG	GTG
S	H	Q	P	D	I	S	S	G	L	E	L	P	F	P	G	V
1035	1044	1053	1062	1071	1080	1089	1098	1107	1116	1125	1134	CCA	CGC	AAC	CTG	CCA
P	T	L	D	N	I	K	N	I	C	H	L	R	R	F	R	S

FIGURE 2C

1143	CAG	CTG	GAG	AGG	GAG	TTC	CAG	CGC	TGC	TGC	CGC	CAG	GGG	AAC	AAT	CAC	ACC	TGT	1188
Q	L	E	R	E	F	Q	R	C	C	R	Q	G	N	N	H	T	C		
1197	ACA	TGG	AAG	GCC	TGG	GAG	GAT	ACC	CTT	GAC	AAA	TAC	TGT	GAC	CGG	GAG	TAT	GCT	1242
T	W	K	A	W	E	D	T	L	D	K	Y	C	D	R	E	Y	A		
1251	GTG	AAG	ACC	CAC	CAC	CAC	TTG	TGT	TGC	CGC	CAC	CCT	CCC	AGC	CCT	ACT	CGG	GAT	1296
V	K	T	H	H	H	L	C	C	R	H	P	P	S	P	T	R	D		
1305	GAG	TGC	TTT	GCC	CGT	CGG	GCT	CCT	TAC	CCC	AAC	TAT	GAC	CGG	GAC	ATC	TTG	ACC	1350
E	C	F	A	R	R	A	P	Y	P	N	Y	D	R	D	I	L	T		
1359	ATT	GAC	ATC	GGT	CGA	GTC	ACC	CCC	AAC	CTC	ATG	GGC	CAC	CTC	TGT	GGA	AAC	CAA	1404
I	D	I	G	R	V	T	P	N	L	M	G	H	L	C	G	N	Q		
1413	AGA	GTT	CTC	ACC	AAG	CAT	AAA	CAT	ATT	CCT	GGG	CTG	ATC	CAC	AAC	ATG	ACT	GCC	1458
R	V	L	T	K	H	K	H	I	P	G	L	I	H	N	M	T	A		
1467	CGC	TGC	TGT	GAC	CTG	CCA	TTT	CCA	GAA	CAG	GGC	TGC	TGT	GCA	GAG	GAG	GAG	AAA	1512
R	C	C	D	L	P	F	P	E	Q	A	C	C	A	E	E	E	K		

FIGURE 2D

TTA	ACC	TTC	ATC	AAT	GAT	CTG	TGT	GGT	CCC	CGA	CGT	AAC	ATC	TGG	CGA	GAC	CCT	
L	T	F	I	N	D	L	C	G	P	R	R	I	W	R	D	P		
1521			1530			1539			1548			1557			1566			
GCC	CTC	TGC	TGT	TAC	CTG	AGT	CCT	GGG	GAT	GAA	CAG	GTC	AAC	TGC	TTC	AAC	ATC	
A	L	C	C	C	Y	L	S	P	G	D	E	Q	V	N	C	F	N	I
1575			1584			1593			1602			1611			1620			
AAT	TAT	CTG	AGG	AAC	GTG	GCT	CTA	GTG	TCT	GGA	GAC	ACT	GAG	AAC	GCC	AAG	GGC	
N	Y	L	R	N	V	A	L	V	S	G	D	T	E	N	A	K	G	
1629			1638			1647			1656			1665			1674			
CAG	GGG	GAG	CAG	GGC	TCA	ACT	GGA	GGA	ACA	AAT	ATC	AGC	TCC	ACC	TCT	GAG	CCC	
Q	G	E	Q	G	S	T	G	G	T	N	I	S	S	T	S	E	P	
1683			1692			1701			1710			1719			1728			
AAG	GAA	GAA	TGA	GTC	ACC	CCA	GAG	CCC	TAG	AGG	GTC	AGA	TGG	GGG	GAA	CCC	CAC	
K	E	E																
1737			1746			1755			1764			1773			1782			
CCT	GCC	CCA	CCC	ATC	TGA	ACA	CTC	ATT	ACA	CTA	AAC	ACC	TCT	TGG	ATT	TGG	TGT	
1791			1800			1809			1818			1827			1836			
CTG	GCC	CAG	G															
1845			1854			1863			1872			1881			1890			
1899																		

FIGURE 2E

1 M P G I K R I L T V T I L A L C L P S P 45517
 1 M A T S G V L P G G G F V A S A A A V A GI 458228

21 G N A Q A Q C T N G F D L D R Q S G Q C 45517
 21 G P E M Q T G R N N F V I R R N P A D - GI 458228

41 L D I D E C R T I P E A C R G D M M C V 45517
 40 - GI 458228

61 N Q N G G Y L C I P R T N P V Y R G P Y 45517
 40 - GI 458228

81 S N P Y S T P Y S G P Y P A A A P P L S 45517
 40 - - - - - - - - - - - - - - - - P Q R GI 458228

101 A P N Y P T I S R P L I C R F G Y Q M D 45517
 43 I P S N P - - S H R I Q C A A G Y E Q S GI 458228

121 E S N O C V D V D E C A T D S H Q C N P 45517
 61 E H N V C Q D I D E C T A G T H N C R A GI 458228

141 T Q I C I N T E G G Y T C S C T D G Y W 45517
 81 D Q V C I N L R G S F A C C Q C P P G Y Q GI 458228

161 L L E G Q C L D I D E C R Y G - Y C Q Q 45517
 101 K R G E Q C V D I D E C T I P P Y C H Q GI 458228

180 L C A N V P G S Y S C T C N P G F T L N 45517
 121 R C V N T P G S F Y C Q C S P G F Q L A GI 458228

200 E D G R S C Q D V N E C A T E N P C V Q 45517
 141 A N N Y T C V D I N E C D A S N Q C A Q GI 458228

220 T C V N T Y G S F I C R C D P G Y E L E 45517
 161 Q C Y N I L G S F I C Q C N Q G Y E L S GI 458228

FIGURE 3A

GS
Glycogen synthase
Glycogen synthase kinase 3
Glycogen synthase kinase 3 beta

240	E D G V H C S D M D E C S F S E F L C Q	45517
181	S D R L N C E D I D E C R T S S Y L C Q	GI 458228
260	H E C V N Q P G T Y F C S C P P G Y I L	45517
201	Y Q C V N E P G K F S C M C P Q G Y Q V	GI 458228
280	L D D N R S C Q D I N E C E H R N H T C	45517
221	V R - S R T C Q D I N E C E T T N E - C	GI 458228
300	N L Q Q T C Y N L Q G G F K C I D P I R	45517
239	R E D E M C W N Y H G G F R C Y P R N P	GI 458228
320	C E E P Y L R I S D N R C M C P A E N P	45517
259	C Q D P Y I L T P E N R C V C P V S N A	GI 458228
340	G C R D Q P F T I L Y R D M D V V S G R	45517
279	M C R E L P Q S I V Y K Y M S I R S D R	GI 458228
360	S V P A D I F Q M Q A T T R Y P G A Y Y	45517
299	S V P S D I F Q I Q A T T I Y A N T I N	GI 458228
380	I F Q I K S G N E G R E F Y M R Q T G P	45517
319	T F R I K S G N E N G E F Y L R Q T S P	GI 458228
400	I S A T L V M T R P I K G P R E I Q L D	45517
339	V S A M L V L V K S L S G P R E H I V D	GI 458228
420	L E M I T V N T V I N F R G S S V I R L	45517
359	L E M L T V S S I G T F R T S S V L R L	GI 458228
440	R I Y V S Q Y P F	45517
379	T I I V G P F S F	GI 458228

FIGURE 3B

1 M G T T A R A A L V L T Y L A V A S A A 1621777
 1 M G T V S R A A L I L A C L A L A S A A GI 496120

21 S E G G F T A T G Q R Q L R P E - - - 1621777
 21 S E G A F K A S D Q R E M T P E R L F Q GI 496120

37 H F Q E V G Y A A P P S P P L S R S L P 1621777
 41 H L H E V G Y A A P P S L P Q T R R L R GI 496120

57 M D H P D S S Q H G P P - F E G Q S Q V 1621777
 61 V D H S V T S L H D P P L F E E Q R E V GI 496120

76 Q P P P P S Q E A T P L Q Q E K L L P A Q 1621777
 81 Q P P S S P E D I P V Y E E D W P T F L GI 496120

96 L P A E K E V G P P L P Q E A V P L Q K 1621777
 101 N P N V D K A G P A V P Q E A I P L Q K GI 496120

116 E L P S L Q - - - - - - - - - H P 1621777
 121 E Q P P P Q V H I E Q K E I D P P A Q P GI 496120

124 N E - - - Q K E G M P A P F G D Q S H P 1621777
 141 Q E E I V Q K E V K P H T L A G Q L P P GI 496120

141 E P E S W N A A Q H C Q Q D R S Q G G W 1621777
 161 E P R T W N P A R H C Q Q G R - R G V W GI 496120

161 G H R L D G F P P G R P S P D N L N Q I 1621777
 180 G H R L D G F P P G R P S P D N L K Q I GI 496120

181 C L P N R Q H V V Y G P W N L P Q S S Y 1621777
 200 C L P E R Q H V I Y G P W N L P Q T G Y GI 496120

201 S H L T R Q G E T L N F L E I G Y S R C 1621777
 220 S H L S R Q G E T L N V L E T G Y S R C GI 496120

FIGURE 4A

221	C H C R S H T N R L E C A K L V W E E A	1621777
240	C P C R S D T N R L D C L K L V W E D A	GI 496120
241	M S R F C E A E F S V K T R P H W C C T	1621777
260	M T Q F C E A E F S V K T R P H L C C R	GI 496120
261	R Q G E A R F S C F Q E E A P Q P H Y Q	1621777
280	L R G E E R F S C F Q K E A P R P D Y L	GI 496120
281	L R A C P S H Q P D I S S G L E L P F P	1621777
300	L R P C P V H Q N G M S S G P Q L P F P	GI 496120
301	P G V P T L D N I K N I C H L R R F R S	1621777
320	P G L P T P D N V K N I C L L R R F R A	GI 496120
321	V P R N L P A T D P L Q R E L L A L I Q	1621777
340	V P R N L P A T D A I Q R Q L Q A L T R	GI 496120
341	L E R E F Q R C C R Q G N N H T C T W K	1621777
360	L E T E F Q R C C R Q G H N H T C T W K	GI 496120
361	A W E D T L D K Y C D R E Y A V K T H H	1621777
380	A W E G T L D G Y C E R E L A I K T H P	GI 496120
381	H L C C R H P P S P T R D E C F A R R A	1621777
400	H S C C H Y P P S P A R D E C F A H L A	GI 496120
401	P Y P N Y D R D I L T I D I G R V T P N	1621777
420	P Y P N Y D R D I L T L D L S R V T P N	GI 496120
421	L M G H L C G N Q R V L T K H K H I P G	1621777
440	L M G Q L C G S G R V L S K H K Q I P G	GI 496120
441	L I H N M T A R C C D L P F P E Q A C C	1621777
460	L I Q N M T V R C C E L P Y P E Q A C C	GI 496120

FIGURE 4B

461 A E E E K L T F I N D L C G P R R N I W 1621777
480 G E E E K L A F I E N L C G P R R N S W GI 496120

481 R D P A L C C Y L S P G D E Q V N C F N 1621777
500 K D P A L C C D L S P E D K Q I N C F N GI 496120

501 I N Y L R N V A L V S G D T E N A K G Q 1621777
520 T N Y L R N V A L V A G D T G N A T G L GI 496120

521 G E Q G S T G G T N I S S T S E P K E E 1621777
540 G E Q G P T R G T D A N P A P G S K E E GI 496120

FIGURE 4C